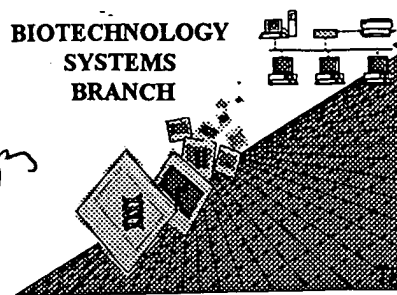


**RAW SEQUENCE LISTING**  
**ERROR REPORT**

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



#7  
RECEIVED

AUG 08 2000

TECH CENTER 1600/2900

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/17/916

Source: 1636

Date Processed by STIC: 7/27/2000

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

**Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

RECEIVED

AUG 08 2000

1636

TECH CENTER 1600/2900

RAW SEQUENCE LISTING      DATE: 07/27/2000  
 PATENT APPLICATION: US/09/171,916      TIME: 13:43:45

Input Set : A:\NAIR-312 Sequence Listing.txt  
 Output Set: N:\CRF3\07272000\I171916.raw

Does Not Comply  
 Corrected Diskette Needed

3 <110> APPLICANT: NAIR, SMITA K.  
 4      BOCZKOWSKI, DAVID J.  
 5      GILBOA, ELI  
 7 <120> TITLE OF INVENTION: METHODS FOR TREATING CANCERS AND PATHOGEN INFECTIONS  
 8      USING ANTIGEN-PRESENTING CELLS LOADED WITH RNA  
 10 <130> FILE REFERENCE: 1579-312  
 12 <140> CURRENT APPLICATION NUMBER: 09/171,916  
 13 <141> CURRENT FILING DATE: 1999-02-16  
 15 <150> PRIOR APPLICATION NUMBER: PCT/US97/07317  
 16 <151> PRIOR FILING DATE: 1997-04-30  
 18 <150> PRIOR APPLICATION NUMBER: 08/640,444  
 19 <151> PRIOR FILING DATE: 1996-04-30  
 21 <160> NUMBER OF SEQ ID NOS: 7  
 23 <170> SOFTWARE: PatentIn Ver. 2.1  
 25 <210> SEQ ID NO: 1  
 26 <211> LENGTH: 4  
 27 <212> TYPE: PRT  
 28 <213> ORGANISM: Artificial Sequence  
 30 <220> FEATURE:  
 31 <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide  
 33 <400> SEQUENCE: 1  
 34 Lys Asp Glu Leu  
 35      1  
 38 <210> SEQ ID NO: 2  
 39 <211> LENGTH: 5  
 40 <212> TYPE: PRT  
 41 <213> ORGANISM: Artificial Sequence  
 43 <220> FEATURE:  
 44 <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide  
 46 <400> SEQUENCE: 2  
 47 Lys Phe Glu Arg Gln  
 48      1                      5  
 51 <210> SEQ ID NO: 3  
 52 <211> LENGTH: 4  
 53 <212> TYPE: PRT  
 54 <213> ORGANISM: Artificial Sequence  
 56 <220> FEATURE:  
 57 <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide  
 59 <400> SEQUENCE: 3  
 60 Gln Arg Glu Lys  
 61      1  
 64 <210> SEQ ID NO: 4  
 65 <211> LENGTH: 25  
 66 <212> TYPE: PRT  
 67 <213> ORGANISM: Artificial Sequence  
 69 <220> FEATURE:  
 70 <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide

pg 1-2

initial response - see circled portion of  
 item 12 on Evan  
 summary sheet -  
 give source of  
 genetic material

RAW SEQUENCE LISTING                      DATE: 07/27/2000  
PATENT APPLICATION:    US/09/171,916              TIME: 13:43:45

Input Set : A:\NAIR-312 Sequence Listing.txt  
Output Set: N:\CRF3\07272000\I171916.raw

72 <400> SEQUENCE: 4  
73 Met Ala Ile Ser Gly Val Pro Val Leu Gly Phe Phe Ile Ile Ala Val  
74    1                      5                      10                      15  
76 Leu Met Ser Ala Gln Glu Ser Trp Ala  
77                      20                      25  
80 <210> SEQ ID NO: 5  
81 <211> LENGTH: 24  
82 <212> TYPE: DNA  
83 <213> ORGANISM: Artificial Sequence  
85 <220> FEATURE:  
86 <223> OTHER INFORMATION: Description of Artificial Sequence: Probe  
88 <400> SEQUENCE: 5  
89 cagtttttca aagttgatta tact                      24  
92 <210> SEQ ID NO: 6  
93 <211> LENGTH: 8  
94 <212> TYPE: PRT  
95 <213> ORGANISM: Artificial Sequence  
97 <220> FEATURE:  
98 <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide  
100 <400> SEQUENCE: 6  
101 Ser Ile Ile Asn Phe Glu Lys Leu  
102    1                      5  
105 <210> SEQ ID NO: 7  
106 <211> LENGTH: 24  
107 <212> TYPE: DNA  
108 <213> ORGANISM: Artificial Sequence  
110 <220> FEATURE:  
111 <223> OTHER INFORMATION: Description of Artificial Sequence: Probe  
113 <400> SEQUENCE: 7  
114 tcatattagt tgaaactttt tgac                      24

VERIFICATION SUMMARY                      DATE: 07/27/2000  
PATENT APPLICATION:    US/09/171,916              TIME: 13:43:46

Input Set : A:\NAIR-312 Sequence Listing.txt  
Output Set: N:\CRF3\07272000\I171916.raw

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/17/96

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1        Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2        Wrapped Aminos      The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3        Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4        Misaligned Amino Acid Numbering      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5        Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6        Variable Length      Sequence(s)        contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7        PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s)       . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8        Skipped Sequences (OLD RULES)      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9        Skipped Sequences (NEW RULES)      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 10        Use of n's or Xaa's (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11        Use of <213>Organism (NEW RULES)      Sequence(s)        are missing this mandatory field or its response.
- 12        Use of <220>Feature (NEW RULES)      Sequence(s)        are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13        PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.